

0570  
10/11

#6

OIEP

P.5

## RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/923,684

TIME: 08:08:29

Input Set : A:\6818-24.ST25.txt

Output Set: N:\CRF3\10042001\I923684.raw

3 <110> APPLICANT: Narayanan, Ramaswamy  
 5 <120> TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER  
 7 <130> FILE REFERENCE: 6818-24

C--&gt; 9 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/923,684

C--&gt; 9 &lt;141&gt; CURRENT FILING DATE: 2001-09-17

9 &lt;160&gt; NUMBER OF SEQ ID NOS: 16

11 &lt;170&gt; SOFTWARE: PatentIn version 3.1

13 &lt;210&gt; SEQ ID NO: 1

14 &lt;211&gt; LENGTH: 3920

15 &lt;212&gt; TYPE: DNA

16 &lt;213&gt; ORGANISM: Homo sapiens

18 &lt;400&gt; SEQUENCE: 1

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23	agaccaggag	ggagaaggaa	aatggcgagt	tttacgagct	tgccaagctg	ctcccgtgc	180
25	cgtcggccat	cacttcgcag	ctggacaaa	cgctccatcat	ccgcctcacc	acgagctacc	240
27	tgaagatgcy	cgccgtcttc	cccgaagggt	taggagacgc	gtggggacag	ccgagccgcg	300
29	ccggggccct	ggacggcgct	gccaaggagc	tgggatcgca	cttgctgcag	actttggatg	360
31	gatttgTTTT	tgtggtagca	tctgatggca	aaatcatgta	tatatccgag	accgcttctg	420
33	tccatttagg	cttatcccag	gtggagctca	cgggcaacag	tatttatgaa	tacatccatc	480
35	cttctgacca	cgatgagatg	accgctgtcc	tcacggccca	ccagccgctg	caccaccacc	540
37	tgctccaaga	gtatgagata	gagaggctgt	tctttcttcg	aatgaaatgt	gtcttggcga	600
39	aaaggaacgc	gggcctgacc	tgcagcggat	acaaggctcat	ccactgcagt	ggctacttga	660
41	agatcaggca	gtatatgctg	gacatgtccc	tgtacgactc	ctgctaccag	attgtggggc	720
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45	acatgttcat	gttcaggggc	agccttgacc	tgaagctgat	attcctggat	tccaggggtga	840
47	ccgaggtgac	gggttacgag	ccgcaggacc	tgatcgagaa	gaccctatac	catcacgtgc	900
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51	tcaccaccaaa	gtactaccgg	ctgctgtcca	agcggggcgg	ctgggtgtgg	gtgcagagct	1020
53	acgccaccgt	ggtgcacaac	agccgctcgt	cccggcccca	ctgcatcgtg	agtgtcaatt	1080
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69	gatccccctg	tgagggtggca	cgctttttcc	tgagcacact	gccagccagc	ggtgaatgcc	1560
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79	ggctggcgct	ggcccgcgcg	gcacccgagt	gctgcgcgcc	cccgaacccc	gaggccccgg	1860
81	gcgcgccggc	gcagctgccc	ttcgtgctgc	tcaactacca	ccgcgtgctg	gcccggcgcg	1920
83	gaccgctggg	ggcgccgcga	cccgcgcgct	ccggcctggc	ctgcgctccc	ggcgggccccg	1980
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ENTERED

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89 ctggccgccc gcgccaggag cctggacccg gcctcccggg gctgcggcgc caccgagccc 2160
91 ggcaaatgcg cacgacctac attaatattat gcagagacag ctgtttgaat tggacccccgc 2220
93 cgccgacttg cggattttcca ccgcggaggc ccgcgcgcgc ggtgccgagg gccgaggagc 2280
95 gcccggttcc gggcaggtga ccgccgcct ctgtcctgcg agggccggtg cgacccagtt 2340
97 gctgggggct tggtttctc accttgaaat cgggcttcac gcgtcttgcc ttgtcccaa 2400
99 cgttcacaaa cagtcccgt gggggattga agcgtttca ctccgcaaat atcctccact 2460
101 ttcaggaggg aaaaccacc ctaccacagt ccgtcttcc aagtggacgg cagacctggg 2520
103 aggggacgcc tgtgtcacga gcccttttag atgcttaggt gaaggcagaa gtgatgattg 2580
105 taagtcccat gaatacacia ctccactgtc tttaaaagtc attcaagagt ctcatattt 2640
107 ttgtttttat ttaacccttt ctccaataca aaaagccaac aaaccaagac taaggggggtg 2700
109 accatgcaat tccattttgt gtctgtgaac atagggtgtgc ttcccaaata cattaacaag 2760
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113 tatattgaat aggcatataa tgcaaaaata tatatgtagc cagacagttt atgagaatga 2880
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117 actaggctcg tgtttgtac aaatagtgtc aataaaagta aattgcacgt gcaatacggg 3000
119 aactgtcaa tggactgcac cttgtgaagg aaaaacatgc ttaagggggg gtaatgaaaa 3060
121 tgatgtagac attttaagca ttttctacac agcgagaaaa cttcgtaaga acatgttacg 3120
123 tgtgcaacag gtaaacagaa atcctttcat aaagcaccag cagtgtttaa aaaatgagct 3180
125 tccattaatt tttacttttt atgggttttg cttaaagatc tcaacatgga aaaatcctgt 3240
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137 aagagtcaca atttgcaaat ttaggaccgt gggtcatgca gcgaaggggc tggatggtag 3600
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141 tgtgtgcaca ggaaataagc cgagggtatt atttttttat gttcatgagt cttgtaatta 3720
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145 taaaagtactg caaaatgctt ttgtgtctac cttgttatta acttttgggg ctgtatttag 3840
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153 <211> LENGTH: 2859
154 <212> TYPE: DNA
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 2
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162 agaccaggag ggagaaggaa aatggcgagt ttacgagct tgccaagctg ctcccgtgc 180
164 cgtcggccat cacttcgcag ctggacaaaag cgtccatcat ccgcctcacc acgagctacc 240
166 tgaagatgcg gcgcgtctc ccgaagggt taggagacgc gtggggacag ccgagccgcg 300
168 ccgggcccct ggacggcgtc gccaaaggagc tgggatcgca cttgctgcag actttggatg 360
170 gatttgtttt tgtggtagca tctgatggca aaatcatgta tatatccgag accgcttctg 420
172 tccatttagg cttatcccag gtggagctca cgggcaacag tatttatgaa tacatccatc 480
174 cttctgacca cgatgagatg accgctgtcc tcacggccca ccagccgctg caccaccacc 540
176 tgctccaaga gtatgagata gagaggtcgt tctttcttcg aatgaaatgt gtcttggcga 600
178 aaaggaacgc gggcctgacc tgcagcggat acaaggtcat ccactgcagt ggctacttga 660
180 agatcaggca gtatatgctg gacatgtccc tgtacgactc ctgctaccag attgtggggc 720
182 tgggtggcgt gggccagtcg ctgccaccca gtgccatcac cgagatcaag ctgtacagta 780

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184 acatgttcat gttcagggcc agccttgacc tgaagctgat attcctggat tccaggggtga      840
186 ccgaggtgac gggttacgag ccgcaggacc tgatcgagaa gacctatac catcacgtgc      900
188 acggctgcga cgtgttccac ctccgctacg cacaccacct cctgttggtg aagggccagg      960
190 tcaccaccaa gtactaccgg ctgctgtcca agcggggcgg ctgggtgtgg gtgcagagct     1020
192 acgccaccgt ggtgcacaac agccgctcgt cccggcccca ctgcatcgtg agtgtcaatt     1080
194 atgtactcac ggagattgaa tacaaggaac ttcagctgtc cctggagcag gtgtccactg     1140
196 ccaagtccca ggactcctgg aggaccgcct tgtctacctc acaagaaact aggaaattag     1200
198 tgaaacccaa aaataccaa atgaagacaa agctgagaac aaacccttac cccccacagc     1260
200 aatacagctc attccaaatg gacaaactgg aatgcggcca gctcggaaaac tggagagcca     1320
202 gtccccctgc aagcgtgctg gtcctccagg aactgcagcc ccaactcagaa agcagtgacc     1380
204 ttctgtacac gccatcctac agcctgccct tctcctacca ttatggacac ttccctctgg     1440
206 actctcactt cttcagcagc aaaaagccaa tgttgccggc caagttcggg cagccccaag     1500
208 gatccccctt tgaggtggca cgctttttcc tgagcacaat gccagccagc ggtgaatgcc     1560
210 agtggcatta tgccaacccc ctagtgccta gcagctcgtc tccagctaaa aatcctccag     1620
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214 tgctcgtggg gaaggtggga ggactgcgca cggccgggag ccgaagcagc catggcgggtg     1740
216 ggtggcagat ggagacagaa ccctcacgct ttgggcaaac ttgccctctt tctgcttcta     1800
218 agtagggctt gctgtgcttt cttgctctca atgcaggtgc tcctcgagag tgagaaatgg     1860
220 cagtctgcct gcctcgggga cactagtgc agtataaagg gcaaaggaaa accgagtatc     1920
222 tggccttcac gtaaatcctg gccacattca ccaaccaaag ggggacagtg attttcaaaa     1980
224 ccagctccca tgtgctgaga acacccagc tgcatttctt ttgcaagatt cctttccact     2040
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228 ggaagtgggg aaaactatgg tggaattttg tgggcttggg gacagaaatg ccactcacca     2160
230 acccagggca aagaacacaa accctccagg cctcagtttc ttcacctgta aaatgggggtg     2220
232 aagctgtgat gtgcctactc ccaaggacac gacacacagt agggacctgc cctgtacatg     2280
234 ctagtccaac agaaaggaat ggcctttcac cttctcctgg tggcaggcaa gcagatgtcc     2340
236 tctgcggaga taccgccagc tccccaggac gcagactgac tcctgtttgc tcgctggacc     2400
238 aaccccaggc agaaggtgga aggtgggaac agaggttttag ctgcaggaca tgtattccca     2460
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242 gccattaaaa tgtgggtgaa ggtgacatca ggattatgtg ccccaggccg ggtcagtggt     2580
244 ctcacacctg taatcccagc actttgggag gccaaaggtg gcggatcacc tgaggtcagg     2640
246 agttttgcac aagcctgcc acaagctgaa accccatctc cactaaaaat acaaaaatta     2700
248 gttgggcatg gtggtgagca cctgtaatcc cagctactct ggaggctgag ataggaggat     2760
250 cacttgaacc cgggaggtgg aggttgcagt gagctaagat cacatcactg cactccagcc     2820
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255 &lt;210&gt; SEQ ID NO: 3

256 &lt;211&gt; LENGTH: 667

257 &lt;212&gt; TYPE: PRT

258 &lt;213&gt; ORGANISM: Homo sapiens

260 &lt;400&gt; SEQUENCE: 3

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263 1 5 10 15
266 Asn Gly Glu Phe Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ser Ala
267 20 25 30
270 Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Thr Ser
271 35 40 45
274 Tyr Leu Lys Met Arg Ala Val Phe Pro Glu Gly Leu Gly Asp Ala Trp
275 50 55 60
278 Gly Gln Pro Ser Arg Ala Gly Pro Leu Asp Gly Val Ala Lys Glu Leu

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279	65					70				75				80		
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283					85					90				95		
286	Ser	Asp	Gly	Lys	Ile	Met	Tyr	Ile	Ser	Glu	Thr	Ala	Ser	Val	His	Leu
287				100					105					110		
290	Gly	Leu	Ser	Gln	Val	Glu	Leu	Thr	Gly	Asn	Ser	Ile	Tyr	Glu	Tyr	Ile
291			115					120					125			
294	His	Pro	Ser	Asp	His	Asp	Glu	Met	Thr	Ala	Val	Leu	Thr	Ala	His	Gln
295		130					135					140				
298	Pro	Leu	His	His	His	Leu	Leu	Gln	Glu	Tyr	Glu	Ile	Glu	Arg	Ser	Phe
299	145					150					155					160
302	Phe	Leu	Arg	Met	Lys	Cys	Val	Leu	Ala	Lys	Arg	Asn	Ala	Gly	Leu	Thr
303					165					170						175
306	Cys	Ser	Gly	Tyr	Lys	Val	Ile	His	Cys	Ser	Gly	Tyr	Leu	Lys	Ile	Arg
307				180					185					190		
310	Gln	Tyr	Met	Leu	Asp	Met	Ser	Leu	Tyr	Asp	Ser	Cys	Tyr	Gln	Ile	Val
311			195					200					205			
314	Gly	Leu	Val	Ala	Val	Gly	Gln	Ser	Leu	Pro	Pro	Ser	Ala	Ile	Thr	Glu
315		210					215					220				
318	Ile	Lys	Leu	Tyr	Ser	Asn	Met	Phe	Met	Phe	Arg	Ala	Ser	Leu	Asp	Leu
319	225					230					235					240
322	Lys	Leu	Ile	Phe	Leu	Asp	Ser	Arg	Val	Thr	Glu	Val	Thr	Gly	Tyr	Glu
323					245					250						255
326	Pro	Gln	Asp	Leu	Ile	Glu	Lys	Thr	Leu	Tyr	His	His	Val	His	Gly	Cys
327				260					265					270		
330	Asp	Val	Phe	His	Leu	Arg	Tyr	Ala	His	His	Leu	Leu	Leu	Val	Lys	Gly
331			275					280					285			
334	Gln	Val	Thr	Thr	Lys	Tyr	Tyr	Arg	Leu	Leu	Ser	Lys	Arg	Gly	Gly	Trp
335		290					295					300				
338	Val	Trp	Val	Gln	Ser	Tyr	Ala	Thr	Val	Val	His	Asn	Ser	Arg	Ser	Ser
339	305					310					315					320
342	Arg	Pro	His	Cys	Ile	Val	Ser	Val	Asn	Tyr	Val	Leu	Thr	Glu	Ile	Glu
343					325					330						335
346	Tyr	Lys	Glu	Leu	Gln	Leu	Ser	Leu	Glu	Gln	Val	Ser	Thr	Ala	Lys	Ser
347				340					345					350		
350	Gln	Asp	Ser	Trp	Arg	Thr	Ala	Leu	Ser	Thr	Ser	Gln	Glu	Thr	Arg	Lys
351			355					360					365			
354	Leu	Val	Lys	Pro	Lys	Asn	Thr	Lys	Met	Lys	Thr	Lys	Leu	Arg	Thr	Asn
355		370					375					380				
358	Pro	Tyr	Pro	Pro	Gln	Gln	Tyr	Ser	Ser	Phe	Gln	Met	Asp	Lys	Leu	Glu
359	385					390					395					400
362	Cys	Gly	Gln	Leu	Gly	Asn	Trp	Arg	Ala	Ser	Pro	Pro	Ala	Ser	Ala	Ala
363					405					410						415
366	Ala	Pro	Pro	Glu	Leu	Gln	Pro	His	Ser	Glu	Ser	Ser	Asp	Leu	Leu	Tyr
367				420					425					430		
370	Thr	Pro	Ser	Tyr	Ser	Leu	Pro	Phe	Ser	Tyr	His	Tyr	Gly	His	Phe	Pro
371			435					440					445			
374	Leu	Asp	Ser	His	Val	Phe	Ser	Ser	Lys	Lys	Pro	Met	Leu	Pro	Ala	Lys
375		450					455					460				

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378 Phe Gly Gln Pro Gln Gly Ser Pro Cys Glu Val Ala Arg Phe Phe Leu
379 465 470 475 480
382 Ser Thr Leu Pro Ala Ser Gly Glu Cys Gln Trp His Tyr Ala Asn Pro
383 485 490 495
386 Leu Val Pro Ser Ser Ser Pro Ala Lys Asn Pro Pro Glu Pro Pro
387 500 505 510
390 Ala Asn Thr Ala Arg His Ser Leu Val Pro Ser Tyr Glu Ala Pro Ala
391 515 520 525
394 Ala Ala Val Arg Arg Phe Gly Glu Asp Thr Ala Pro Pro Ser Phe Pro
395 530 535 540
398 Ser Cys Gly His Tyr Arg Glu Glu Pro Ala Leu Gly Pro Ala Lys Ala
399 545 550 555 560
402 Ala Arg Gln Ala Ala Arg Asp Gly Ala Arg Leu Ala Leu Ala Arg Ala
403 565 570 575
406 Ala Pro Glu Cys Cys Ala Pro Pro Thr Pro Glu Ala Pro Gly Ala Pro
407 580 585 590
410 Ala Gln Leu Pro Phe Val Leu Leu Asn Tyr His Arg Val Leu Ala Arg
411 595 600 605
414 Arg Gly Pro Leu Gly Gly Ala Ala Pro Ala Ala Ser Gly Leu Ala Cys
415 610 615 620
418 Ala Pro Gly Gly Pro Glu Ala Ala Thr Gly Ala Leu Arg Leu Arg His
419 625 630 635 640
422 Pro Ser Pro Ala Ala Thr Ser Pro Pro Gly Ala Pro Leu Pro His Tyr
423 645 650 655
426 Leu Gly Ala Ser Val Ile Ile Thr Asn Gly Arg
427 660 665
430 <210> SEQ ID NO: 4
431 <211> LENGTH: 570
432 <212> TYPE: PRT
433 <213> ORGANISM: Homo sapiens
435 <400> SEQUENCE: 4
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438 1 5 10 15
441 Asn Gly Glu Phe Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ser Ala
442 20 25 30
445 Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Thr Ser
446 35 40 45
449 Tyr Leu Lys Met Arg Ala Val Phe Pro Glu Gly Leu Gly Asp Ala Trp
450 50 55 60
453 Gly Gln Pro Ser Arg Ala Gly Pro Leu Asp Gly Val Ala Lys Glu Leu
454 65 70 75 80
457 Gly Ser His Leu Leu Gln Thr Leu Asp Gly Phe Val Phe Val Val Ala
458 85 90 95
461 Ser Asp Gly Lys Ile Met Tyr Ile Ser Glu Thr Ala Ser Val His Leu
462 100 105 110
465 Gly Leu Ser Gln Val Glu Leu Thr Gly Asn Ser Ile Tyr Glu Tyr Ile
466 115 120 125
469 His Pro Ser Asp His Asp Glu Met Thr Ala Val Leu Thr Ala His Gln
470 130 135 140

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\6818-24.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5